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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/881,736

DATE: 07/30/2001  
TIME: 15:53:55

Input Set : A:\0652 2260001 seq list.txt  
Output Set: N:\CRF3\07302001\I881736.raw

ENTERED

5 <110> APPLICANT: Glotzer, Michael  
6 Jantsch-Plunger, Verena  
7 Romano, Alper  
8 Mishima, Masanori  
9 Kaitna, Susanne  
11 <120> TITLE OF INVENTION: Cyk-4 polypeptides, DNA molecules encoding them and their  
use in  
12 screening methods  
14 <130> FILE REFERENCE: 0652.2260001/EKS/AES  
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/881,736  
C--> 17 <141> CURRENT FILING DATE: 2001-06-18  
19 <150> PRIOR APPLICATION NUMBER: EP 00 112 880.0  
20 <151> PRIOR FILING DATE: 2000-06-19  
22 <150> PRIOR APPLICATION NUMBER: EP 01 110 554.1  
23 <151> PRIOR FILING DATE: 2001-04-30  
25 <150> PRIOR APPLICATION NUMBER: 60/241,231  
26 <151> PRIOR FILING DATE: 2000-10-18  
28 <150> PRIOR APPLICATION NUMBER: To be determined  
29 <151> PRIOR FILING DATE: 2001-06-13  
32 <160> NUMBER OF SEQ ID NOS: 6  
34 <170> SOFTWARE: PatentIn Ver. 2.1  
38 <210> SEQ ID NO: 1  
39 <211> LENGTH: 3050  
40 <212> TYPE: DNA  
41 <213> ORGANISM: Homo sapiens  
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45 <222> LOCATION: (1)..(70)  
47 <220> FEATURE:  
48 <221> NAME/KEY: CDS  
49 <222> LOCATION: (71)..(1969)  
51 <220> FEATURE:  
52 <221> NAME/KEY: 3'UTR  
53 <222> LOCATION: (1970)..(3050)  
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60 cgtgtgaaag atg gat act atg atg ctg aat gtg cgg aat ctg ttt gag 109  
62 Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu  
63 1 5 10  
65 cag ctt gtg cgc cgg gtg gag att ctc agt gaa gga aat gaa gtc caa 157  
67 Gln Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln  
68 15 20 25  
70 ttt atc cag ttg gcg aag gac ttt gag gat ttc cgt aaa aag tgg cag 205  
72 Phe Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln  
73 30 35 40 45  
75 agg act gac cat gag ctg ggg aaa tac aag gat ctt ttg atg aaa gca 253  
77 Arg Thr Asp His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala  
78 50 55 60

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80	gag act gag cga agt gct ctg gat gtt aag ctg aag cat gca cgt aat	301
82	Glu Thr Glu Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn	
83	65 70 75	
85	cag gtg gat gta gag atc aaa cgg aga cag aga gct gag gct gac tgc	349
87	Gln Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys	
88	80 85 90	
90	gaa aag ctg gaa cga cag att cag ctg att cga gag atg ctc atg tgt	397
92	Glu Lys Leu Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys	
93	95 100 105	
95	gac aca tct ggc agc att caa cta agc gag gag caa aaa tca gct ctg	445
97	Asp Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu	
98	110 115 120 125	
100	gct ttt ctc aac aga ggc caa cca tcc agc agc aat gct ggg aac aaa	493
102	Ala Phe Leu Asn Arg Gly Gln Pro Ser Ser Asn Ala Gly Asn Lys	
103	130 135 140	
105	aga cta tca acc att gat gaa tct ggt tcc att tta tca gat atc agc	541
107	Arg Leu Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser	
108	145 150 155	
110	ttt gac aag act gat gaa tca ctg gat tgg gac tct tct ttg gtg aag	589
112	Phe Asp Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys	
113	160 165 170	
115	act ttc aaa ctg aag aag aga gaa aag agg cgc tct act agc cga cag	637
117	Thr Phe Lys Leu Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln	
118	175 180 185	
120	ttt gtt gat ggt ccc cct gga cct gta aag aaa act cgt tcc att ggc	685
122	Phe Val Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly	
123	190 195 200 205	
125	tct gca gta gac cag ggg aat gaa tcc ata gtt gca aaa act aca gtg	733
127	Ser Ala Val Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val	
128	210 215 220	
130	act gtt ccc aat gat ggc ggg ccc atc gaa gct gtg tcc act att gag	781
132	Thr Val Pro Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu	
133	225 230 235	
135	act gtg cca tat tgg acc agg agc cga agg aaa aca ggt act tta caa	829
137	Thr Val Pro Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln	
138	240 245 250	
140	cct tgg aac agt gac tcc acc ctg aac agc agg cag ctg gag cca aga	877
142	Pro Trp Asn Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg	
143	255 260 265	
145	act gag aca gac agt gtg ggc acg cca cag agt aat gga ggg atg cgc	925
147	Thr Glu Thr Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg	
148	270 275 280 285	
150	ctg cat gac ttt gtt tct aag acg gtt att aaa cct gaa tcc tgt gtt	973
152	Leu His Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val	
153	290 295 300	
155	cca tgt gga aag cgg ata aaa ttt ggc aaa tta tct ctg aag tgt cga	1021
157	Pro Cys Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg	
158	305 310 315	
160	gac tgt cgt gtg gtc tct cat cca gaa tgt cgg gac cgc tgt ccc ctt	1069

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162	Asp Cys Arg Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu			
163	320	325	330	
165	ccc tgc att cct acc ctg ata gga aca cct gtc aag att gga gag gga	1117		
167	Pro Cys Ile Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly			
168	335	340	345	
170	atg ctg gca gac ttt gtg tcc ca <sup>g</sup> act tct cca atg atc ccc tcc att	1165		
172	Met Leu Ala Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile			
173	350	355	360	365
175	gtt gtg cat tgt gta aat gag att gag caa aga ggt ctg act gag aca	1213		
177	Val Val His Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr			
178	370	375	380	
180	ggc ctg tat agg atc tct ggc tgt gac cgc aca gta aaa gag ctg aaa	1261		
182	Gly Leu Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys			
183	385	390	395	
185	gag aaa ttc ctc aga gtg aaa act gta ccc ctc ctc agc aaa gtg gat	1309		
187	Glu Lys Phe Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp			
188	400	405	410	
190	gat atc cat gct atc tgt agc ctt cta aaa gac ttt ctt cga aac ctc	1357		
192	Asp Ile His Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu			
193	415	420	425	
195	aaa gaa cct ctt ctg acc ttt cgc ctt aac aga gcc ttt atg gaa gca	1405		
197	Lys Glu Pro Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala			
198	430	435	440	445
200	gca gaa atc aca gat gaa gac aac agc ata gct gcc atg tac caa gct	1453		
202	Ala Glu Ile Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala			
203	450	455	460	
205	gtt ggt gaa ctg ccc cag gcc aac agg gac aca tta gct ttc ctc atg	1501		
207	Val Gly Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met			
208	465	470	475	
210	att cac ttg cag aga gtg gct cag agt cca cat act aaa atg gat gtt	1549		
212	Ile His Leu Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val			
213	480	485	490	
215	gcc aat ctg gct aaa gtc ttt ggc cct aca ata gtg gcc cat gct gtg	1597		
217	Ala Asn Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val			
218	495	500	505	
220	ccc aat cca gac cca gtg aca atg tca cag gac atc aag cgt caa ccc	1645		
222	Pro Asn Pro Asp Pro Val Thr Met Ser Gln Asp Ile Lys Arg Gln Pro			
223	510	515	520	525
225	aag gtg gtt gag cgc ctg ctt tcc ttg cct ctg gag tat tgg agt cag	1693		
227	Lys Val Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Ser Gln			
228	530	535	540	
230	tcc atg atg gtg gag caa gag aac att gac ccc cta cat gtc att gaa	1741		
232	Phe Met Met Val Glu Gln Glu Asn Ile Asp Pro Leu His Val Ile Glu			
233	545	550	555	
235	aac tca aat gcc ttt tca aca cca cag aca cca gat att aaa gtg agt	1789		
237	Asn Ser Asn Ala Phe Ser Thr Pro Gln Thr Pro Asp Ile Lys Val Ser			
238	560	565	570	
240	tta ctg gga cct gtg acc act cct gaa cat cag ctt ctc aag act cct	1837		
242	Leu Leu Gly Pro Val Thr Pro Glu His Gln Leu Lys Thr Pro			

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243	575	580	585														
245	tca	tct	agt	tcc	ctg	tca	cag	aga	gtc	cgt	tcc	acc	ctc	acc	aag	aac	1885
247	Ser	Ser	Ser	Ser	Leu	Ser	Gln	Arg	Val	Arg	Ser	Thr	Leu	Thr	Lys	Asn	
248	590		595						600						605		
250	act	cct	aga	ttt	ggg	agc	aaa	agc	aag	tct	gcc	act	aac	cta	gga	cga	1933
252	Thr	Pro	Arg	Phe	Gly	Ser	Lys	Ser	Lys	Ser	Ala	Thr	Asn	Leu	Gly	Arg	
253									610			615			620		
255	caa	ggc	aac	ttt	ttt	gct	tct	cca	atg	ctc	aag	tga	agt	cac	atct		1979
257	Gln	Gly	Asn	Phe	Phe	Ala	Ser	Pro	Met	Leu	Lys						
258						625					630						
260	gcctgttact	tcccagcatt	gactgactat	aagaaaggac	acatctgtac	tctgctctgc											2039
263	agcctcctgt	actcattact	acttttagca	tttccaggc	ttttactcaa	gtttaattgt											2099
266	gcatgaggt	tttattaaaa	ctatataat	ctccccttcc	ttctcctcaa	gtcacataat											2159
269	atcagcactt	tgtgctggc	attgttggga	gcttttagat	gagacatctt	tccaggggta											2219
272	gaagggttag	tatgaaattt	gttgtgattc	tttttggga	agggggttat	tgttcctttg											2279
275	gcttaaagcc	aaatgctgct	catagaatga	tctttctcta	gtttcattta	gaactgattt											2339
278	ccgtgagaca	atgacagaaa	ccctacctat	ctgataagat	tagcttgct	cagggtggga											2399
281	agtgggaggg	cagggcaaag	aaaggattag	accagaggat	ttaggatgcc	tccttctaag											2459
284	aaccagaagt	tctcattccc	cattatgaac	tgagctataa	tatggagctt	tcataaaaaat											2519
287	gggatgcatt	gaggacagaa	ctagtatgg	gagttatgcgt	agctttgatt	tggatgatta											2579
290	ggtcttaat	agtgttgagt	ggcacaacct	tgtaaatgtg	aaagtacaac	tcgtattttat											2639
293	ctctgatgt	ccgtggctg	aactttgggt	tcattttgggg	tcaaagccag	tttttctttt											2699
296	aaaattgaat	tcattctgt	gcttggccccc	cataccccc	accttgc	gtggagccca											2759
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305	tggatgctga	aattttccc	atgaaacata	gccacatcta	gatagatgt	agctttttct											2939
308	tctgttaaaa	ttattcttaa	tgtctgtaaa	aacgattttc	ttctgtagaa	tgtttgactt											2999
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327					20			25			30						
329	Leu	Ala	Lys	Asp	Phe	Glu	Asp	Phe	Arg	Lys	Lys	Trp	Gln	Arg	Thr	Asp	
330					35			40			45						
332	His	Glu	Leu	Gly	Lys	Tyr	Lys	Asp	Leu	Leu	Met	Lys	Ala	Glu	Thr	Glu	
333					50			55			60						
335	Arg	Ser	Ala	Leu	Asp	Val	Lys	Leu	Lys	His	Ala	Arg	Asn	Gln	Val	Asp	
336					65			70			75			80			
338	Val	Glu	Ile	Lys	Arg	Arg	Gln	Arg	Ala	Glu	Ala	Asp	Cys	Glu	Lys	Leu	
339					85			90			95						
341	Glu	Arg	Gln	Ile	Gln	Leu	Ile	Arg	Glu	Met	Leu	Met	Cys	Asp	Thr	Ser	
342					100			105			110						
344	Gly	Ser	Ile	Gln	Leu	Ser	Glu	Glu	Gln	Lys	Ser	Ala	Leu	Ala	Phe	Leu	
345					115			120			125						

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347 Asn Arg Gly Gln Pro Ser Ser Asn Ala Gly Asn Lys Arg Leu Ser  
 348 130 135 140  
 350 Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp Lys  
 351 145 150 155 160  
 353 Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr Phe Lys  
 354 165 170 175  
 356 Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln Phe Val Asp  
 357 180 185 190  
 359 Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly Ser Ala Val  
 360 195 200 205  
 362 Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val Pro  
 363 210 215 220  
 365 Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Val Pro  
 366 225 230 235 240  
 368 Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln Pro Trp Asn  
 369 245 250 255  
 371 Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg Thr Glu Thr  
 372 260 265 270  
 374 Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu His Asp  
 375 275 280 285  
 377 Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro Cys Gly  
 378 290 295 300  
 380 Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys Arg  
 381 305 310 315 320  
 383 Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys Ile  
 384 325 330 335  
 386 Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu Ala  
 387 340 345 350  
 389 Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile Val Val His  
 390 355 360 365  
 392 Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr Gly Leu Tyr  
 393 370 375 380  
 395 Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys Phe  
 396 385 390 395 400  
 398 Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile His  
 399 405 410 415  
 401 Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu Pro  
 402 420 425 430  
 404 Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala Glu Ile  
 405 435 440 445  
 407 Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala Val Gly Glu  
 408 450 455 460  
 410 Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile His Leu  
 411 465 470 475 480  
 413 Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val Ala Asn Leu  
 414 485 490 495  
 416 Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val Pro Asn Pro  
 417 500 505 510  
 419 Asp Pro Val Thr Met Ser Gln Asp Ile Lys Arg Gln Pro Lys Val Val

**VERIFICATION SUMMARY**

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Input Set : A:\0652 2260001 seq list.txt  
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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date